

196219.ST25.txt  
SEQUENCE LISTING

<110> May, Gregory  
Baszczyński, Christopher  
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Mahajan, Pramod

<120> PLANT MSH2 SEQUENCES AND METHODS OF USE

<130> 5839-2 (035839/196219)

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<170> PatentIn version 3.0

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99 Leu Pro Glu Leu Lys Leu Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser  
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147 Phe Phe Lys Thr Leu Pro Lys Asp Pro Arg Ala Val Arg Leu Phe Asp  
30 35 40  
cgt cggtt gac tat tat aca tct cat gga gat gat gca act ttc att gca  
195 Arg Arg Asp Tyr Tyr Ser His Gly Asp Asp Ala Thr Phe Ile Ala  
45 50 55  
gag aca tat tac cac aca aca act gcg tta c<sup>c</sup>ga cag ttg ggt aat aga  
243 Glu Thr Tyr Tyr His Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg  
60 65 70  
gct gat gcc ctt tcc agt gtt agt gtg agt aga aac atg ttt gaa aca  
291 Ala Asp Ala Leu Ser Ser Val Ser Val Ser Arg Asn Met Phe Glu Thr  
75 80 85 90  
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339 Ile Ala Arg Asp Ile Leu Leu Glu Arg Met Asp Arg Thr Leu Glu Leu

95

100

105

tat gag ggc agt ggt tca aac tgg aga ctg gta aaa agt gga acc cca  
 387

Tyr Glu Gly Ser Gly Ser Asn Trp Arg Leu Val Lys Ser Gly Thr Pro  
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ggg aat ctt gga agt ttt gag gat att ctg ttt gct aat aat gaa atg  
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Gly Asn Leu Gly Ser Phe Glu Asp Ile Leu Phe Ala Asn Asn Glu Met  
 125 130 135

caa aat tct ccg gtg att gct gct ctt gct cca aac ttc ggt cag aat  
 483

Gln Asn Ser Pro Val Ile Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn  
 140 145 150

gga tgt gaa gtt ggc tta ggc tat gtt gat att act aag aga gtc ctt  
 531

Gly Cys Glu Val Gly Leu Gly Tyr Val Asp Ile Thr Lys Arg Val Leu  
 155 160 165 170

ggt tta aca gaa ttt cta gat gat agc cac ttc aca aat ttg gag tct  
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Gly Leu Thr Glu Phe Leu Asp Asp Ser His Phe Thr Asn Leu Glu Ser  
 175 180 185

gct ttg gtt gct ctt ggt tgc aga gaa tgt ctt gta cca gcg gag act  
 627

Ala Leu Val Ala Leu Gly Cys Arg Glu Cys Leu Val Pro Ala Glu Thr  
 190 195 200

ggc aaa tcc agt gaa tac agg cct atg ttt gat gca ata tct aga tgc  
 675

Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys  
 205 210 215

ggc gtg atg gta act gaa aga aag aaa act gaa ttt aaa ggg aga gat  
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Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp  
 220 225 230

ttg gta cag gat ctt ggt agg ctc gtc aag ggt tca gta gaa cct gtt  
 771

Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val  
 235 240 245 250

cga gat ttg gtc tct ggg ttc gaa tgt gca tca ggc gct ttg ggg tgc  
 819

Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys  
 255 260 265

ata ctt tct tat gca gaa cta ctt gcg gat gag agc aac tat gga aac  
 867

Ile Leu Ser Tyr Ala Glu Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn  
 270 275 280

tat aca gtc aaa caa tac aac ctc aat agt tac atg aga tta gat tct  
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Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser  
 285 290 295

gct gct atg aga gca ctg aat gtt atg gag agc aaa tca gat gct aat  
 963

Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn  
 300 305 310

aaa aat ttt agc ttg ttc ggt ctg atg aat aga acg tgt act gct gga  
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Lys Asn Phe Ser Leu Phe Gly Leu Met Asn Arg Thr Cys Thr Ala Gly  
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atg ggt aaa agg tta ttg cac atg tgg ctg aag caa cct tta cta gat  
 1059

Met Gly Lys Arg Leu Leu His Met Trp Leu Lys Gln Pro Leu Leu Asp  
 335 340 345

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 1107

Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu  
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 1155

Asp Ala Ala Leu Arg Gln Asp Leu Arg Gln His Leu Lys Arg Ile Ser  
 365 370 375

gat att gag cgg ctg aca cac aat ctt gag agg aaa aga gcc agt tta  
 1203

Asp Ile Glu Arg Leu Thr His Asn Leu Glu Arg Lys Arg Ala Ser Leu  
 380 385 390

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 1251

Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile  
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 1299

Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg  
 415 420 425

gaa agg tat att gat tct cta gag aaa tgg agt gat gat aat cac ctg  
 1347

Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu  
 430 435 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt  
 1395

Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu  
 445 450 455

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 1443

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1491  
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1539  
His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu  
495 500 505  
  
aaa cta gat aaa gaa aca caa ttt gga cac gtc ttc aga att acc aag  
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Lys Leu Asp Lys Glu Thr Gln Phe Gly His Val Phe Arg Ile Thr Lys  
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aaa gaa gaa cca aaa gtc agg aag cag cta aat tct cac tac att gtt  
1635  
Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val  
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ctc gaa aca cgt aag gat ggg gta aag ttc acc tat aca aaa ctc aaa  
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Leu Glu Thr Arg Lys Asp Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys  
540 545 550  
  
aaa cta gga gat cag ttc cag aag att gta gag gag tac aaa agc tgt  
1731  
Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys  
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cag aaa gaa ttg gta gct cgt gta gtt caa aca gct gcg agt ttc tcc  
1779  
Gln Lys Glu Leu Val Ala Arg Val Val Gln Thr Ala Ala Ser Phe Ser  
575 580 585  
  
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1827  
Glu Val Phe Ala Gly Ile Ala Gly Val Leu Ala Glu Leu Asp Val Leu  
590 595 600  
  
ctg agt ttt gcg gat ttg gct gcc agt tgc cca act ccc tac aca aga  
1875  
Leu Ser Phe Ala Asp Leu Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg  
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cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt  
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Pro Asn Ile Ser Pro Pro Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys  
620 625 630  
  
agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat  
1971  
Arg His Pro Cys Val Glu Ala Gln Asp Trp Val Asn Ser Ile Pro Asn  
635 640 645 650  
  
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655 660 665

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cct aac atg ggt gga aag tcg acc tac att cgg cag gtt ggt gtg aat  
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 Pro Asn Met Gly Gly Lys Ser Thr Tyr Ile Arg Gln Val Gly Val Asn  
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gtc ctg atg gcc caa gtt ggc tcg ttt gtt cca tgt gac aat gct acc  
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 Val Leu Met Ala Gln Val Gly Ser Phe Val Pro Cys Asp Asn Ala Thr  
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att tct att cgt gat tgt att ttt gct cgt gtt ggc gct gga gat tgc  
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 Ile Ser Ile Arg Asp Cys Ile Phe Ala Arg Val Gly Ala Gly Asp Cys  
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cag ctg aga gga gtt tct act ttt atg caa gag atg ctt gag act gca  
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tcg atc ttg aaa gga gct act gat aga tca ttg att ata att gat gag  
 2259  
 Ser Ile Leu Lys Gly Ala Thr Asp Arg Ser Leu Ile Ile Asp Glu  
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 750 755 760

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 2355  
 Ile Cys Glu His Ile Val Glu Ile Lys Ala Pro Thr Leu Phe Ala  
 765 770 775

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 Thr His Phe His Glu Leu Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn  
 780 785 790

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 2451  
 Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His  
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 Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro  
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 845 850 855

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gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt  
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Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly  
875 880 885 890

act gcc aga gct cgg caa ttc tta cag gat ttc gct cag ttg cca ctg  
2739  
Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu  
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2787  
Asp Lys Met Asp Pro Asn Val Val Arg Gln Lys Leu Ser Lys Met Lys  
910 915 920

acc gac ctg gag agg gat gca gtt gac tct cac tgg ctt cag caa ttc  
2835  
Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe  
925 930 935

ttt taattcttca gattagaact atcttctatt ctgtgaagct tgggggggaa  
2888  
Phe

tgatacttat gggtttgtg gatataactt agcctatctg taaactttca tttaaatcct  
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Lys Asp Pro Arg Ala Val Arg Leu Phe Asp Arg Arg Asp Tyr Tyr Thr  
35 40 45

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Ser His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr  
50 55 60

Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser  
65 70 75 80

Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu  
85 90 95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser  
100 105 110

Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe  
115 120 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile  
130 135 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu  
145 150 155 160

Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu  
165 170 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly  
180 185 190

Cys Arg Glu Cys Leu Val Pro Ala Glu Thr Gly Lys Ser Ser Glu Tyr  
195 200 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu  
210 215 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly  
225 230 235 240

Arg Leu Val Lys Gly Ser Val Glu Pro Val Arg Asp Leu Val Ser Gly  
245 250 255

Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys Ile Leu Ser Tyr Ala Glu  
260 265 270

Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn Tyr Thr Val Lys Gln Tyr  
275 280 285

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Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser Ala Ala Met Arg Ala Leu  
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Asn Val Met Glu Ser Lys Ser Asp Ala Asn Lys Asn Phe Ser Leu Phe  
305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu  
325 330 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys  
340 345 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln  
355 360 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Ile Glu Arg Leu Thr  
370 375 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu  
385 390 395 400

Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile Lys Ser Val Leu Glu Arg  
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His Asp Gly Gln Phe Ala Thr Leu Ile Arg Glu Arg Tyr Ile Asp Ser  
420 425 430

Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu  
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Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met  
450 455 460

Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln  
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Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn  
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Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu Lys Leu Asp Lys Glu Thr  
500 505 510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val

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515 520 525

Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp  
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Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe  
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Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys Gln Lys Glu Leu Val Ala  
565 570 575

Arg Val Val Gln Thr Ala Ala Ser Phe Ser Glu Val Phe Ala Gly Ile  
580 585 590

Ala Gly Val Leu Ala Glu Leu Asp Val Leu Leu Ser Phe Ala Asp Leu  
595 600 605

Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg Pro Asn Ile Ser Pro Pro  
610 615 620

Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys Arg His Pro Cys Val Glu  
625 630 635 640

Ala Gln Asp Trp Val Asn Ser Ile Pro Asn Asp Cys Arg Leu Val Arg  
645 650 655

Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys  
660 665 670

Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val  
675 680 685

Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys  
690 695 700

Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser  
705 710 715 720

Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala  
725 730 735

Thr Asp Arg Ser Leu Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser  
740 745 750

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Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Ile Val  
755 760 765

Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu  
770 775 780

Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala  
785 790 795 800

Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg  
805 810 815

Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser  
820 825 830

Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val  
835 840 845

Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile  
850 855 860

Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg  
865 870 875 880

Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln  
885 890 895

Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu Asp Lys Met Asp Pro Asn  
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Val Val Arg Gln Lys Leu Ser Lys Met Lys Thr Asp Leu Glu Arg Asp  
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Ala Val Asp Ser His Trp Leu Gln Gln Phe Phe  
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## 196219.ST25.txt

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99

Leu	Pro	Glu	Leu	Lys	Leu	Asp	Ala	Lys	Gln	Ala	Gln	Gly	Phe	Leu	Ser
								15		20				25	

ttt ttc aaa acc cta ccc aag gac cct agg gca gtt cgc ctc ttt gat  
147

Phe	Phe	Lys	Thr	Leu	Pro	Lys	Asp	Pro	Arg	Ala	Val	Arg	Leu	Phe	Asp
								30		35			40		

cgt cggt gac tat tat act gct cat gga gat gat gca act ttc att gca  
195

Arg	Arg	Asp	Tyr	Tyr	Thr	Ala	His	Gly	Asp	Asp	Ala	Thr	Phe	Ile	Ala
							45		50			55			

gag aca tat tac cac aca aca act gcg tta cga cag ttg ggt aat aga  
243

Glu	Thr	Tyr	Tyr	His	Thr	Thr	Ala	Leu	Arg	Gln	Leu	Gly	Asn	Arg
							60		65		70			

gct gat gcc ctt tcc agt gtt agt gtg agt aga aac atg ttt gaa aca  
291

Ala	Asp	Ala	Leu	Ser	Ser	Val	Ser	Val	Ser	Arg	Asn	Met	Phe	Glu	Thr
							75		80		85		90		

ata gct cgt gac att ctc ttg gag aga atg gac cgt act ctt gaa cta  
339

Ile	Ala	Arg	Asp	Ile	Leu	Leu	Glu	Arg	Met	Asp	Arg	Thr	Leu	Glu	Leu
							95		100			105			

tat gag ggc agt ggt tca aac tgg aga ctg gta aaa agt gga acc cca  
387

Tyr	Glu	Gly	Ser	Gly	Ser	Asn	Trp	Arg	Leu	Val	Lys	Ser	Gly	Thr	Pro
							110		115			120			

ggg aat ctt gga agt ttt gag gat att ctg ttt gct aat aat gaa atg  
435

Gly	Asn	Leu	Gly	Ser	Phe	Glu	Asp	Ile	Leu	Phe	Ala	Asn	Asn	Glu	Met
							125		130		135				

caa aat tct ccg gtg att gct gct ctt gct cca aac ttc ggt cag aat  
483

Gln	Asn	Ser	Pro	Val	Ile	Ala	Ala	Leu	Ala	Pro	Asn	Phe	Gly	Gln	Asn
							140		145		150				

gga tgt gaa gtt ggc tta ggc tat gtt gat att act aag aga gtc ctt  
531

Gly	Cys	Glu	Val	Gly	Leu	Gly	Tyr	Val	Asp	Ile	Thr	Lys	Arg	Val	Leu
							155		160		165		170		

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579

Gly	Leu	Thr	Glu	Phe	Leu	Asp	Asp	Ser	His	Phe	Thr	Asn	Leu	Glu	Ser
								175		180		185			

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gct ttg gtt gct ctt ggt tgc aga gaa tgt ctt gta cca gcg gag act  
 627  
 Ala Leu Val Ala Leu Gly Cys Arg Glu Cys Leu Val Pro Ala Glu Thr  
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 ggc aaa tcc agt gaa tac agg cct atg ttt gat gca ata tct aga tgc  
 675  
 Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys  
 205 210 215  
  
 ggc gtg atg gta act gaa aga aag aaa act gaa ttt aaa ggg aga gat  
 723  
 Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp  
 220 225 230  
  
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 771  
 Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val  
 235 240 245 250  
  
 cga gat ttg gtc tct ggg ttc gaa tgt gca tca ggc gct ttg ggg tgc  
 819  
 Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys  
 255 260 265  
  
 ata ctt tct tat gca gaa cta ctt gcg gat gag agc aac tat gga aac  
 867  
 Ile Leu Ser Tyr Ala Glu Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn  
 270 275 280  
  
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 915  
 Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser  
 285 290 295  
  
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 963  
 Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn  
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 aaa aat ttt agc ttg ttc ggt ctg atg aat aga acg tgt act gct gga  
 1011  
 Lys Asn Phe Ser Leu Phe Gly Leu Met Asn Arg Thr Cys Thr Ala Gly  
 315 320 325 330  
  
 atg ggt aaa agg tta ttg cac atg tgg ctg aag caa cct tta cta gat  
 1059  
 Met Gly Lys Arg Leu Leu His Met Trp Leu Lys Gln Pro Leu Leu Asp  
 335 340 345  
  
 gta gaa gag att aac tgt agg ctg gat tta gtt caa tca ttc gtg gag  
 1107  
 Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu  
 350 355 360  
  
 gat gct gcg ctt cgc caa gat ttg agg cag cat ctg aaa aga att tca  
 1155  
 Asp Ala Ala Leu Arg Gln Asp Leu Arg Gln His Leu Lys Arg Ile Ser  
 365 370 375

196219.ST25.txt

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1203  
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380 385 390

gtg cac gtt gta aaa ctc tat cag tca agt acc aga gta cca tat atc  
1251  
Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile  
395 400 405 410

aaa agt gtt ttg gaa cgt cat gat ggg caa ttt gca aca ctc atc agg  
1299  
Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg  
415 420 425

gaa agg tat att gat tct cta gag aaa tgg agt gat gat aat cac ctg  
1347  
Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu  
430 435 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt  
1395  
Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu  
445 450 455

gag aat gga gaa tac atg att tct tct gca tat gac cca aat tta tct  
1443  
Glu Asn Gly Glu Tyr Met Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser  
460 465 470

gct ctg aag gat gag caa gag aca ttg gag cga caa att cat aat ttg  
1491  
Ala Leu Lys Asp Glu Gln Glu Thr Leu Glu Arg Gln Ile His Asn Leu  
475 480 485 490

cac aaa caa act gcc aat gat ctt gat cta cct att gat aag tca ctt  
1539  
His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu  
495 500 505

aaa cta gat aaa gaa aca caa ttt gga cac gtc ttc aga att acc aag  
1587  
Lys Leu Asp Lys Glu Thr Gln Phe Gly His Val Phe Arg Ile Thr Lys  
510 515 520

aaa gaa gaa cca aaa gtc agg aag cag cta aat tct cac tac att gtt  
1635  
Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val  
525 530 535

ctc gaa aca cgt aag gat ggg gta aag ttc acc tat aca aaa ctc aaa  
1683  
Leu Glu Thr Arg Lys Asp Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys  
540 545 550

aaa cta gga gat cag ttc cag aag att gta gag gag tac aaa agc tgt  
1731  
Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys

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555	560	565	570													
cag aaa gaa ttg gta gct cgt gta gtt caa aca gct gcg agt ttc tcc 1779																
Gln	Lys	Glu	Leu	Val	Ala	Arg	Val	Val	Gln	Thr	Ala	Ala	Ser	Phe	Ser	
gag gtg ttt gca ggt ata gct ggt gta ctt gct gag ttg gat gtg tta 1827																
Glu	Val	Phe	Ala	Gly	Ile	Ala	Gly	Val	Leu	Ala	Glu	Leu	Asp	Val	Leu	
ctg agt ttt gcg gat ttg gct gcc agt tgc cca act ccc tac aca aga 1875																
Leu	Ser	Phe	Ala	Asp	Leu	Ala	Ala	Ser	Cys	Pro	Thr	Pro	Tyr	Thr	Arg	
cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt 1923																
Pro	Asn	Ile	Ser	Pro	Pro	Asp	Thr	Gly	Asp	Ile	Ile	Leu	Glu	Gly	Cys	
agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat 1971																
Arg	His	Pro	Cys	Val	Glu	Ala	Gln	Asp	Trp	Val	Asn	Ser	Ile	Pro	Asn	
gac tgt aga cta gtt agg gga gag agt tgg ttt cag att atc aca ggc 2019																
Asp	Cys	Arg	Leu	Val	Arg	Gly	Glu	Ser	Trp	Phe	Gln	Ile	Ile	Thr	Gly	
cct aac atg ggt gga aag tcg acc tac att cgg cag gtt ggt gtg aat 2067																
Pro	Asn	Met	Gly	Gly	Lys	Ser	Thr	Tyr	Ile	Arg	Gln	Val	Gly	Val	Asn	
gtc ctg atg gcc caa gtt ggc tcg ttt gtt cca tgt gac aat gct acc 2115																
Val	Leu	Met	Ala	Gln	Val	Gly	Ser	Phe	Val	Pro	Cys	Asp	Asn	Ala	Thr	
att tct att cgt gat tgt att ttt gct cgt gtt ggc gct gga gat tgc 2163																
Ile	Ser	Ile	Arg	Asp	Cys	Ile	Phe	Ala	Arg	Val	Gly	Ala	Gly	Asp	Cys	
cag ctg aga gga gtt tct act ttt atg caa gag atg ctt gag act gca 2211																
Gln	Leu	Arg	Gly	Val	Ser	Thr	Phe	Met	Gln	Glu	Met	Leu	Glu	Thr	Ala	
tcg atc ttg aaa gga gct act gat aga tca ttg att ata att gat gag 2259																
Ser	Ile	Leu	Lys	Gly	Ala	Thr	Asp	Arg	Ser	Leu	Ile	Ile	Ile	Asp	Glu	
ttg ggc cgt ggg aca tca acc tac gat ggc ttt ggt tta gct tgg gct 2307																

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Leu Gly Arg Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala  
750 755 760

att tgt gag cac att gtt gaa gaa att aaa gca cca aca ttg ttt gcc  
2355

Ile Cys Glu His Ile Val Glu Ile Lys Ala Pro Thr Leu Phe Ala  
765 770 775

act cac ttt cat gag ctg act gca tta gcc aac aag aat gga gac aat  
2403

Thr His Phe His Glu Leu Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn  
780 785 790

gga cat aag aaa aat gct ggg ata gca aat ttt cat gtt ttt gca cac  
2451

Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His  
795 800 805 810

att gac cct tct aat cgc aag cta act atg ctt tac aag gtt cac cca  
2499

Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro  
815 820 825

ggt gct tgt gat cag agt ttt ggt att cat gtt gct gaa ttt gca aat  
2547

Gly Ala Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu Phe Ala Asn  
830 835 840

ttt cca ccg agt gtt gtg gct ctg gct aga gaa aag gca tct gag ttg  
2595

Phe Pro Pro Ser Val Val Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu  
845 850 855

gag gat ttc tct cct att gcc ata att cca aat gac att aaa gag gca  
2643

Glu Asp Phe Ser Pro Ile Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala  
860 865 870

gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt  
2691

Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly  
875 880 885 890

act gcc aga gct cgg caa ttc tta cag gat ttc gct cag ttg cca ctg  
2739

Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu  
895 900 905

gat aag atg gat cca aac gtc agg caa aag ttg agc aaa atg aaa  
2787

Asp Lys Met Asp Pro Asn Val Val Arg Gln Lys Leu Ser Lys Met Lys  
910 915 920

acc gac ctg gag agg gat gca gtt gac tct cac tgg ctt cag caa ttc  
2835

Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe  
925 930 935

ttt taattcttca gattagaact atcttctatt ctgtgaagct tgggggggaa

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2888  
Phe

tgatacttat gggtttgtg gatataactt agcctatctg taaactttca tttaaatcct  
2948

taccccaaac atgattctct gtaatcaggg gactttgtg tgcattctgt gttaatagta  
3008

agcgttatct tatatggtca aaaaa  
3033

<210> 4

<211> 939

<212> PRT

<213> Nicotiana tabacum

<400> 4

Met Asn Glu Asn Leu Glu Glu Gln Ser Lys Leu Pro Glu Leu Lys Leu  
1 5 10 15

Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser Phe Phe Lys Thr Leu Pro  
20 25 30

Lys Asp Pro Arg Ala Val Arg Leu Phe Asp Arg Arg Asp Tyr Tyr Thr  
35 40 45

Ala His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr  
50 55 60

Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser  
65 70 75 80

Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu  
85 90 95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser  
100 105 110

Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe  
115 120 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile  
130 135 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu  
145 150 155 160

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Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu  
165 170 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly  
180 185 190

Cys Arg Glu Cys Leu Val Pro Ala Glu Thr Gly Lys Ser Ser Glu Tyr  
195 200 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu  
210 215 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly  
225 230 235 240

Arg Leu Val Lys Gly Ser Val Glu Pro Val Arg Asp Leu Val Ser Gly  
245 250 255

Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys Ile Leu Ser Tyr Ala Glu  
260 265 270

Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn Tyr Thr Val Lys Gln Tyr  
275 280 285

Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser Ala Ala Met Arg Ala Leu  
290 295 300

Asn Val Met Glu Ser Lys Ser Asp Ala Asn Lys Asn Phe Ser Leu Phe  
305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu  
325 330 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys  
340 345 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln  
355 360 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Ile Glu Arg Leu Thr  
370 375 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu

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385	390	395	400
Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile Lys Ser Val Leu Glu Arg			
405	410	415	
His Asp Gly Gln Phe Ala Thr Leu Ile Arg Glu Arg Tyr Ile Asp Ser			
420	425	430	
Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu			
435	440	445	
Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met			
450	455	460	
Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln			
465	470	475	480
Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn			
485	490	495	
Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu Lys Leu Asp Lys Glu Thr			
500	505	510	
Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val			
515	520	525	
Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp			
530	535	540	
Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe			
545	550	555	560
Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys Gln Lys Glu Leu Val Ala			
565	570	575	
Arg Val Val Gln Thr Ala Ala Ser Phe Ser Glu Val Phe Ala Gly Ile			
580	585	590	
Ala Gly Val Leu Ala Glu Leu Asp Val Leu Leu Ser Phe Ala Asp Leu			
595	600	605	
Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg Pro Asn Ile Ser Pro Pro			
610	615	620	

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Asp	Thr	Gly	Asp	Ile	Ile	Leu	Glu	Gly	Cys	Arg	His	Pro	Cys	Val	Glu
625				630			635							640	
Ala Gln Asp Trp Val Asn Ser Ile Pro Asn Asp Cys Arg Leu Val Arg															
				645			650							655	
Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys															
				660			665							670	
Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val															
				675			680							685	
Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys															
				690			695							700	
Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser															
				705			710							720	
Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala															
				725			730							735	
Thr Asp Arg Ser Leu Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser															
				740			745							750	
Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Ile Val															
				755			760							765	
Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu															
				770			775							780	
Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala															
				785			790							800	
Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg															
				805			810							815	
Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser															
				820			825							830	
Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val															
				835			840							845	
Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile															
				850			855							860	

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Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg  
865 870 875 880

Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln  
885 890 895

Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu Asp Lys Met Asp Pro Asn  
900 905 910

Val Val Arg Gln Lys Leu Ser Lys Met Lys Thr Asp Leu Glu Arg Asp  
915 920 925

Ala Val Asp Ser His Trp Leu Gln Gln Phe Phe  
930 935

<210> 5  
<211> 160  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 5  
nnagagaatc ttctcttagct cccgcattt ctctttcccg ccaaccacata tccctccatt  
60

ttccccattttc tctataaaat cctttgttt tcatttctac tgccggaaaat ttaaaagaaaa  
120

aaaaaaaaatg aatgaaaatt tggaggaaca gagcaagctt  
160

<210> 6  
<211> 163  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>  
<221> unsure  
<222> (141)..(141)  
<223> "n" at position 141 can be A, C, G, or T

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<400> 6  
nnaagagaat cttctctagc tccccccat tctttccc gccaaccac atccctccat  
60  
  
tttccatta ctctataaaa tccttgctt ttcatattcta ctgcagaaaa gttaaagaa  
120  
  
aaaaaaaaat gaatgaaaat ntggaggaac agagcaagct tca  
163

<210> 7  
<211> 163  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 7  
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacaca tccctccgtt  
60  
  
ttcccattac tctataaaaat ccttgcttt tcatttctac tgcaaaaaag ttaaaagaaaa  
120  
  
aaaaaaaaaa tgaatgaaaa ttggaggaa cagagcaagc ttc  
163

<210> 8  
<211> 165  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>  
<221> unsure  
<222> (161)..(161)  
<223> "n" at position 161 can be A, C, G, or T

<400> 8  
nnttctctag ctcccccggcca ttctctttcc cgccaatcca aatccctcca ttttcctcta  
60  
  
ttttccatt actctataaa atcctttcct tttcatttct acagcataaa ggttaaagaa  
120  
  
aaaaaaaaatga atgaaaattt ggaggaacag agcaagttca ncgaa

165

<210> 9  
<211> 166  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (165)..(166)  
<223> "n" at positions 165 abd 166 can be A, C, G, or T

<400> 9  
agagaatctt ctctagctcc cgccattctt cttcccgcc aatccaagtc cctccatTTT  
60  
cctctatTTT cccattactc tataaaatcc ttccctttc atttctacag cataaaggTT  
120  
aaagaaaaaa aaatgaatga aaattggag gaacagagca agctnn  
166

<210> 10  
<211> 166  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 10  
nnagagaatc ttctctagct cccgcattt ctcttcccg ccaaccaca tcacctccatt  
60  
ttcccattac tctataaaat ccTTTGTttt tcatttctac tgcaaaaaAG ttAAAAGAAA  
120  
aaaaaaaaatg aatgaaaatt tggaggaaca gagcaagctt caatcg  
166

<210> 11  
<211> 166  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>

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<221> unsure  
<222> (157)..(158)  
<223> "n" at positions 157 and 158 can be A, C, G, or T

<400> 11  
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacataccatt  
60  
  
ttcccattac tctataaaat cctttgctt tcatttctac tgcagaaaag ttaaaagaaa  
120  
  
aaaaaaaaatg aatgaaaatttggaggaaca gagcaanntt caatcg  
166

<210> 12  
<211> 165  
<212> DNA  
<213> Nicotiana tabacum  
  
<220>  
<221> unsure  
<222> (1)..(2)  
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 12  
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacataccatt  
60  
  
ttcccattac tctataaaat cctttgctt tcatttctac tgcagaaaag ttaaaagaaa  
120  
  
aaaaaatgaa tgaaaatttg gaggaacaga gcaagcttca atcga  
165

<210> 13  
<211> 314  
<212> DNA  
<213> Nicotiana tabacum  
  
<220>  
<221> unsure  
<222> (222)..(222)  
<223> "n" at position 222 can be A, C, G, or T

<400> 13  
gatatcacta gtgattcttt gcaatgaaag ttgcacatc tccatgagca gtataatagt  
60  
  
cccgacgatc aaagaggcga actgccctag ggtccttggg tagggtttg aaaaatgaga  
120  
  
gaaatccttg agcttgctta gcatcaagtt taagctcagg aagcttgctc tgccctcca  
180

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aaatcgaatt cccgcggccg ccatggcgcc cgggagcatg cnacgtcggg cccaattcgc  
240

cctatagtga gtcgttattac aattcaactgg ccgtcgaaaa acaacgtcgt gactggaaa  
300

accctggcgta tacc  
314

<210> 14  
<211> 314  
<212> DNA  
<213> Nicotiana tabacum

<400> 14  
gatatacacta gtgattcttt gcaatgaaag ttgcacatc tccatgagca gtataatagt  
60

ccgcacgatc aaagaggcgaa actgccttag ggtccttggg cagggtttt aagaatgaga  
120

gaaatccttg agcttgctta gcatccagtt taagctcggg aagcttgctc tgttcctcca  
180

aaatcgaatt cccgcggccg ccatggcgcc cgggagcatg ccgacgtcgg gcccattcgc  
240

ccctatagtg agtcgttattaa caattcaactg gccgtcgaaaa tacaacgtcgt tgactggaaa  
300

aaccctggcgta ttac  
314

<210> 15  
<211> 311  
<212> DNA  
<213> Nicotiana tabacum

<400> 15  
atatacactag tgattcttg caatgaaagt tgcacatct ccatgagatg tataatagtc  
60

ccgacgatca aagaggcgaa ctgccttagg gtccttggg agggtttga agaatgagag  
120

aaatccttgaa gcttgcttag catccagttt aagctcggga agcttgctc tgttcctccaa  
180

aatcgaattc ccgcggccgc catggcgccg gggagcatgc gacgtcgggc ccaattcgcc  
240

ctatagtgag tcgttattaca attcaactggc cgtcgaaaa caacgtcgtg actggaaa  
300

ccctggcgta a  
311

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<210> 16  
<211> 214  
<212> DNA  
<213> Nicotiana tabacum

<400> 16  
gttaaacctt aattcgtaa atgtttatt acatttcag aagtttattc ttacaagtct  
60

tttctagtc taattttta ttatTTactt tttctttca tattatTTat tggTTTaat  
120

aaatAGAGGG ttcatattAG ttgTTcagCT gatTTAGGGA tttaaccgta gtttgattga  
180

ttgaaatTTt ttaCCgtgaa tggTTTTgtt tttag  
214

<210> 17  
<211> 223  
<212> DNA  
<213> Nicotiana tabacum

<400> 17  
gtaaaacctt aattcttga atgTTTattt acatttcag aagtttattc ttacaagctt  
60

ttttctagtt ctaatTTTT ttatTTata gttttctct ttatattgtt tactgtgttt  
120

aataaaatggA tattgatggT tcataTTAGC ggttcaactg atttggggat ttaactgtAG  
180

tttGATTGAT tgatatttGT tattgtGAAT ggtcttGTTT tag  
223

<210> 18  
<211> 222  
<212> DNA  
<213> Nicotiana tabacum

<400> 18  
gtaaaacctt aattcttga atgTTTattt acatttcag aagtttattc ttacaagctt  
60

ttttctagtt ctaatTTTT ttatTTata gttttctct ttatattgtt tactgtgttt  
120

aataaaatggA tattgatggT tcataTTAGC ggttcaactg atttggggat ttaactgtAG  
180

tttGATTGAT gatatttGTT attgtGAATg gttttGTTT ag  
222

<210> 19

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<211> 107  
<212> DNA  
<213> Nicotiana tabacum

<400> 19  
gtaactttt catattattc attctgttta aatagttatt gcacccac ttgttagagaa  
60  
  
aattgctcg cggttcactt aatagagaac ttttgatttt ttgcag  
107

<210> 20  
<211> 105  
<212> DNA  
<213> Nicotiana tabacum

<400> 20  
gtaactttt catattattc attctgttta aatagttatt gcacccac ttgttagagaa  
60  
  
aattgttagt cggttgctt aatagagaac tccttttt tgca  
105

<210> 21  
<211> 106  
<212> DNA  
<213> Nicotiana tabacum

<220>  
<221> unsure  
<222> (11)..(16)  
<223> "n" at positions 11-16 can be A, C, G, or T

<400> 21  
gttaactttt nnnnnnattc attctgttca aacggttatt gcacccac ttgttagagaa  
60  
  
aattgttagt cggttgctt aatagagaac tccttttt ttgcag  
106

<210> 22  
<211> 5  
<212> PRT  
<213> MutS consensus sequence

<400> 22  
  
Thr Gly Pro Asn Met  
1 5

<210> 23  
<211> 5  
<212> PRT  
<213> MutS consensus sequence

<400> 23

Phe Ala Thr His Tyr  
1 5

<210> 24

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 24

gtaacagggc ctaacatggg  
20

<210> 25

<211> 19

<212> DNA

<213> oligonucleotide primer

<400> 25

ggaagttagt agcaaacag  
19

<210> 26

<211> 19

<212> DNA

<213> oligonucleotide primer

<400> 26

caggccctaa catgggtgg  
19

<210> 27

<211> 20

<212> DNA

<213> oligonucleotide primer

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